



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stocco, Douglas M.
Clark, Barbara J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION OF
STEROIDOGENESIS

(iii) NUMBER OF SEQUENCES: 19

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(E) COUNTRY: U.S.A.
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:
(B) COMPUTER:
(C) OPERATING SYSTEM:
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 33,732
(C) REFERENCE/DOCKET NUMBER: 043375.0006/DLM

(ix) TELECOMMUNICATION INFORMATION:

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5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACCCAC GCGTCCGCTC AGGACCTTGA AAGGCTCAGG AAGAACAACC CTTGAGCACC 60

20 TCAGCACTCA GCATGTTCTT CGCTACGTTT AAGCTGTGTG CTGGAAGCTC CTATAGACAT 120

ATGCGGAATA TGAAAGGATT AAGGCACCAA GCTGTGCTGG CCATTGGCCA AGAGCTCAAC 180

TGGAGAGCAC TGGGGGATTC CAGTCCCGGG TGGATGGGTC AAGTTCGACG TCGGAGCTCT 240

25 CTGCTTGGTT CTCAACTGGA AGCAACACTC TATAGTGACC AGGAGCTGTC CTACATCCAG 300

CAGGGAGAGG TGGCTATGCA GAAGGCCTTG GGCATACTCA ACAACCAGGA AGGCTGGAAG 360

30 AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GTGCTAAGTA AGATGGTGCC AGATGTGGGC 420

AAGGTGTTTC GCTTGGAGGT GGTGGTAGAC CAGCCCATGG ACAGACTCTA TGAAGAACTT 480

GTGGACCGCA TGGAGGCCAT GGGAGAGTGG AACCCAAATG TCAAGGAGAT CAAGGTCCTG 540

35 CAGAGGATTG GAAAAGACAC GGTCATCACT CATGAGCTGG CTGCGGCGGC AGCAGGCAAC 600

CTGGTGGGGC CTCGAGACTT CGTGAGCGTG CGCTGTACCA AGCGCAGAGG TTCCACCTGT 660

GTGCTGGCAG GCATGGCCAC ACATTTTGGG GAGATGCCGG AGCAGAGTGG TGTCATCAGA 720

5 GCTGAACACG GCCCCACCTG CATGGTGCTT CATCCACTGG CTGGAAGTCC CTCCAAGACT 780

AAACTCACTT GGCTGCTCAG TATTGACCTG AAGGGGTGGC TGCCGAAGAC AATCATCAAC 840

CAGGTCCTAT CGCAGACCCA GATAGAGTTC GCCAACCACC TGCGCAAGCG CCTGGAAGCC 900

10 AGCCCTGCCT CTGAGGCCCA GTGTTAAGGA CTGTCCACCA CATTGACCTG CAAATCATTG 960

GAAGCTCTCA CAGGAAGCCT GCAAGTCTGT CCATCTTCAG CTAACAGCAT CGGGAGGGGT 1020

15 GGTAGTCAGG AGACACTAGG ACTGACTGGT AAAATCAGGA TCAGCAAAAT AGAAATGAGG 1080

CTTAGAATAA AAGTTCTCTA GTGTCTCCCA CTGCATAGCT GTGAAGGCTA AGGGATAAGT 1140

AGCTATGAAA CCTTTCATCT AGGCTTGTAT ATGCTGACCT AAAAGACACC AGCAGCTACG 1200

20 AACAGGGGAT GCTAAGGATC GGGAACTGTT GTCTTACCAG CTCCAAATGT CACTACCTGA 1260

AGGCAGTGTG CACACAAAGC AAGGTCTTGC CTAGGAAACT CTGTAAAAGT TCTCCTCTGT 1320

25 AAAAGGCCAG AACTTGAATG AACTACCTA CAAAGGGCCT TTCCAGAGTA TTCCAACTTT 1380

TCTCTGAGGA GAAATGAAAC CATCATTGTG CCGACTTCCC TACTAATCCC ATGACAATAA 1440

AGAACATACA TAAAAAAAAA AAAAAA 1466

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10	M F L A T F K L C A G S S Y R H	
	Met Phe Leu Ala Thr Phe Lys Leu Cys Ala Gly Ser Ser Tyr Arg His	
	1 5 10 15	
	M R N M L G L R H Q A V L A I G	
	Met Arg Asn Met Lys Gly Leu Arg His Gln Ala Val Leu Ala Ile Gly	
	20 25 30	
15	G E L N W R A L G D S S P G W M	
	Gln Glu Leu Asn Trp Arg Ala Leu Gly Asp Ser Ser Pro Gly Trp Met	
	35 40 45	
	G Q V R R R S S L L G S Q L E A	
	Gly Gln Val Arg Arg Arg Ser Ser Leu Leu Gly Ser Gln Leu Glu Ala	
	50 55 60	
20	T L Y S D Q E L S Y I Q Q G E V	
	Thr Leu Tyr Ser Asp Gln Glu Leu Ser Tyr Ile Gln Gln Gly Glu Val	
	65 70 75 80	
	A M Q K A L G I L N N Q E G W K	
	Ala Met Gln Lys Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys	
25	85 90 95	
	K E S Q Q E N G D E V L S K M V	
	Lys Glu Ser Gln Gln Glu Asn Gly Asp Glu Val Leu Ser Lys Met Val	
	100 105 110	
30	P D V G K V F R L E V V V D Q P	
	Pro Asp Val Gly Lys Val Phe Arg Leu Glu Val Val Val Asp Gln Pro	
	115 120 125	
	M D K L Y E E L V D R M E A M G	
	Met Asp Arg Leu Tyr Glu Glu Leu Val Asp Arg Met Glu Ala Met Gly	
	130 135 140	

35

E W N P N V K E I K V L Q R I G
 Glu Trp Asn Pro Asn Val Lys Glu Ile Lys Val Leu Gln Arg Ile Gly
 145 150 155 160
 K D T V I T H E L A A A A A G N
 Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Gly Asn
 5 165 170 175
 L V G P K D F V S V R C T K K K
 Leu Val Gly Pro Arg Asp Phe Val Ser Val Arg Cys Thr Lys Arg Arg
 180 185 190
 G S T C V L A G M A T H F G E M
 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
 10 195 200 205
 P E Q S G V I R A E H G P T C M
 Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met
 210 215 220
 V L H P L A G S P S K T K L T W
 Val Leu His Pro Leu Ala Gly Ser Pro Ser Lys Thr Lys Leu Thr Trp
 15 225 230 235 240
 L L S I D L K G W L P K T I I N
 Leu Leu Ser Ile Asp Leu Lys Gly Trp Leu Pro Lys Thr Ile Ile Asn
 20 245 250 255
 Q V L S G T Q I E E A N H L R K
 Gln Val Leu Ser Gln Thr Gln Ile Glu Phe Ala Asn His Leu Arg Lys
 260 265 270
 R L E A S P A S E A Q C
 Arg Leu Glu Ala Ser Pro Ala Ser Glu Ala Gln Cys
 25 275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

(2) INFORMATION FOR SEQ ID NO:4:

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

^G ^S ^T ^C ^V ^L ^A ^G ^M ^A ^T ^H ^F ^G ^E ^M
 Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met
 1 5 10 15

^P ^E ^Q
 Pro Glu Gln

5

(2) INFORMATION FOR SEQ ID NO:6:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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^N ^Q ^E ^G ^W ^K
 Asn Gln Glu Gly Trp Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:7:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35

A E H G P T C M V
Ala Glu His Gly Pro Thr Cys Met Val

1

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5 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

I L N N Q E G W K K E
Ile Leu Asn Asn Gln Glu Gly Trp Lys Lys Glu
1 5 10

20 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

30

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: one-of(3, 12, 15, 18)

(D) OTHER INFORMATION: /mod_base= OTHER

35 /note= "N = (A or C or G or T/U) or (unknown or other)"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 6

(D) OTHER INFORMATION: /mod_base= OTHER

5 /note= "R = A or G"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: one-of(9, 21)

10 (D) OTHER INFORMATION: /mod_base= OTHER

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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GCNGARCAYG GNCCNACNTG YATGG

25

(2) INFORMATION FOR SEQ ID NO:10:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

30

(A) NAME/KEY: modified_base

(B) LOCATION: one-of(5, 17)

(D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

35

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: one-of(8, 11, 14, 23)
(D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = (A or C or G or T/U) or (unknown or other)"

5

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: 20
(D) OTHER INFORMATION: /mod_base= OTHER

10

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATRCANGT NGGNC CRTGY TCNGC

25

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

(A) NAME/KEY: modified_base
(B) LOCATION: 3
(D) OTHER INFORMATION: /mod_base= OTHER

30

/note= "Y = C or T/U"

(ix) FEATURE:

35

(A) NAME/KEY: modified_base

(B) LOCATION: one-of(6, 9)

(D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

5 (ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 12

(D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = (A or C or G or T/U) or (unknown or other)"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAYCARCARG GNTGGAA

17

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

20

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCCANCCYT CYTGRTT

17

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10	AACCAGGAAG GCTGGAAGAA GGAAAGCCAG CAGGAGAACG GGGACGAAGT GCTAAGTAAG	60
	ATGGTGCCAG ATGTGGGCAA GGTGTTTCGC TTGGAGGTGG TGGTAGACCA GCCCATGGAC	120
	AGACTCTATG AAGAACTTGT GGACCGCATG GAGGCCATGG GAGAGTGGAA CCCAAATGTC	180
15	AAGGAGATCA AGGTCCTGCA GAGGATTGGA AAAGACACGG TCATCACTCA TGAGCTGGCT	240
	GCGGCGGCAG CAGGCAACCT GGTGGGGCCT CGAGACTTCG TGAGCGTGCG CTGTACCAAG	300
20	CGCAGAGGTT CCACCTGTGT GCTGGCAGGC ATGGCCACAC ATTTTGGGGA GATGCCGGAG	360
	CAGAGTGGTG TCATCAGAGC TGAACACGGC CCCACCTGCA T	401

25 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "RNA"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

	GUCGACCCAC GCGUCCGCUC AGGACCUUGA AAGGCUCAGG AAGAACAACC CUUGAGCACC	60
5	UCAGCACUCA GCAUGUUCU CGCUACGUUC AAGCUGUGUG CUGGAAGCUC CUAUAGACAU	120
	AUGCGGAAUA UGAAAGGAUU AAGGCACCAA GCUGUGCUGG CCAUUGGCCA AGAGCUCAAC	180
	UGGAGAGCAC UGGGGGAUUC CAGUCCCGGG UGGAUGGGUC AAGUUCGACG UCGGAGCUCU	240
10	CUGCUUGGUU CUCAACUGGA AGCAACACUC UAUAGUGACC AGGAGCUGUC CUACAUCCAG	300
	CAGGGAGAGG UGGCUAUGCA GAAGGCTUUG GGCAUACUCA ACAACCAGGA AGGCUGGAAG	360
15	AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GUGCUAAGUA AGAUGGUGCC AGAUGUGGGC	420
	AAGGUGUUUC GCUUGGAGGU GGUGGUAGAC CAGCCCAUGG ACAGACUCUA UGAAGAACUU	480
	GUGGACCGCA UGGAGGCCAU GGGAGAGUGG AACCCTAAUG UCAAGGAGAU CAAGGUCCUG	540
20	CAGAGGAUUG GAAAAGACAC GGUCAUCACU CAUGAGCUGG CUGCGGCGGC AGCAGGCAAC	600
	CUGGUGGGGC CUCGAGACUU CGUGAGCGUG CGCUGUACCA AGCGCAGAGG UUCCACCUGU	660
25	GUGCUGGCAG GCAUGGCCAC ACAUUUUGGG GAGAUGCCGG AGCAGAGUGG UGUCAUCAGA	720
	GCUGAACACG GCCCCACCTG CAUGGUGCUU CAUCCACUGG CUGGAAGUCC CUCCAAGACU	780
	AAACUCACUU GGCUGCUCAG UAUUGACCUG AAGGGGUGGC UGCCGAAGAC AAUCAUCAAC	840
30	CAGGUCCUUAU CGCAGACCCA GAUAGAGUUC GCCAACCACC UGCGCAAGCG CCUGGAAGCC	900
	AGCCUGCCU CUGAGGCCCA GUGUUAAGGA CUGUCCACCA CAUUGACCUG CAAUCAUUG	960
35	GAAGCUCUCA CAGGAAGCCU GCAAGUCUGU CCAUCUUCAG CUAACAGCAU CGGGAGGGGU	1020

	GGUAGUCAGG AGACACUAGG ACUGACUGGU AAAAUCAGGA UCAGCAAAAU AGAAAUGAGG	1080
	CUUAGAAUAA AAGUUCUCUA GUGUCUCCCA CUGCAUAGCU GUGAAGGCUA AGGGAUAAAGU	1140
5	AGCUAUGAAA CCUUUCAUCU AGGCUUGUAU AUGCUGACCU AAAAGACACC AGCAGCUACG	1200
	AACAGGGGAU GCUAAGGAUC GGGAACUGUU GUCUUACCAG CUCCAAAUGU CACUACCUGA	1260
	AGGCAGUGUG CACACAAAGC AAGGUCUUGC CUAGGAAACU CUGUAAAAGU UCUCCUCUGU	1320
10	AAAAGGCCAG AACUUGAUG AAACUACCUA CAAAGGGCCU UCCAGAGUA UUCAACUUU	1380
	UCUCUGAGGA GAAUGAAAC CAUCAUUGUG CCGACUCCCC UACUAAUCCC AUGACAAUAA	1440
15	AGAACAUACA UAAAAAAAAA AAAAAA	1466

(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

25 (ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:15:

30	267 GTGGATTAAC CAGGTTCGGC GCGGAGCTC TCTACTCGGT TCTCGGCTGG AAGAGACTCT	326
	327 CTACAGTGAC CAGGAGCTGG CCTATCTCCA GCAGGGGGAG GAGGCCATGC AGAAGGCCTT	386
	387 GGGCATCCTT AGCAACCAAG AGGGCTGGAA GAAGGAGAGT CAGCAGGACA ATGGGGACAA	446
	447 AGTGATGAGT AAAGTGGTCC CAGATGTGGG CAAGGTGTTC CGGCTGGAGG TCGTGGTGGA	506
35	507 CCAGCCCATG GAGAGGCTCT ATGAAGAGCT CGTGGAGCGC ATGGAAGCAA TGGGGGAGTG	566

567 GAACCCCAAT GTCAAGGAGA TCAAGGTCCT GCAGAAGATC GGAAAAGATA CATTATTAC 626
 627 TCACGAGCTG GCTGCCGAGG CAGCAGGAAA CCTGGTG GGGG CCCCCTGACT TTGTGAGCGT 686
 687 GCGCTGTGCC AAGCGCCGAG GCTCCACCTG TGTGCTGGCT GGCATGGACA CAGACTTCGG 746
 747 GAACATGCCT GAGCAGAAGG GTGTCATCAG GGCGGAGCAC GGTCCCACCTT GCATGGTGCT 806
 5 807 TCACCCGTTG GCTGGAAGTC CCTCTAAGAC CAAACTTACG TGGCTACTCA GCATCGACCT 866
 867 CAAGGGGTGG CTGCCCAAGA GCATCATCAA CCAGGTCCTG TCCCAGACCC AGGTGGATTT 926
 927 TGCCAACCAC CTGCGCAAGC GCCTGGAGTC CCACCCTGCC TCTGAAGCCA GGTGTTGAAG 986
 987 AC 988

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

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(B) TYPE:

(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

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(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:16:

127 ATGCTGCTAG CGACATTCAA GCTGTGCGCT GGGAGCTCCT ACAGACACAT GCGCAACATG 186
 25 187 AAGGGGCTGA GGCAACAGGC TGTGATGGCC ATCAGCCAGG AGCTGAACCG GAGGGCCCTG 246
 247 GGGGGCCCCA CCCC 260

(2) INFORMATION FOR SEQ ID NO:17:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

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(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:17:

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1051 ACTGGAAGCC TGCAAGTCT 1069

(2) INFORMATION FOR SEQ ID NO:18:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

15

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

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SEQUENCE DESCRIPTION: SEQ ID NO:18:

1	MLLATFKLCA GSSYRHRNM KGLRQQAVMA ISQELNRRAL GGPTPSTWIN	50
51	QVRRRSSLLG SRLEETLYSD QELAYLQQGE EAMQKALGIL SNQEGWKES	100
101	QQDNGDKVMS KVPDVGKVF RLEVVDQPM ERLYEELVER MEAMGEWNP	150
25	151 VKEIKVLQKI GKDTFITHL AABAAGNLVG PRDFVSVRCA KRGSTCVLA	200
	201 GMATDFGNMP EQKGVIRAEH GPTCMVLHPL AGSPSKTKLT WLLSIDLKGW	250
	251 LPKSIINQVL SQTQVDFANHL RKRLESHA SEARC	285

(2) INFORMATION FOR SEQ ID NO:19:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

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(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:19:

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agaacaccag gtccaggctg cagctgcggg actcagaggc gaacgttgag gggctcagga 60
aggacgaaga accacccttg agagaagagg cagcagcagc gcggcagcag cagcggcagc 120
gacccccacca ctgccacatt tgccaggaaa caATGCTGCT AGCGACATTC AAGCTGTGCG 180
CTGGGAGCTC CTACAGACAC ATGCGCAACA TGAAGGGGCT GAGGCAACAG GCTGTGATGG 240
CCATCAGCCA GGAGCTGAAC CGGAGGGCCC TGGGGGGCCC CACCCTAGC ACGTGGATTA 300
ACCAGGTTCTG GCGGCGGAGC TCTCTACTCG GTTCTCGGCT GGAAGAGACT CTCTACAGTG 360
ACCAGGAGCT GGCCTATCTC CAGCAGGGGG AGGAGGCCAT GCAGAAGGCC TTGGGCATCC 420
TTAGCAACCA AGAGGGCTGG AAGAAGGAGA GTCAGCAGGA CAATGGGGAC AAAGTGATGA 480
GTAAAGTGGT CCCAGATGTG GGCAAGGTGT TCCGGCTGGA GGTCGTGGTG GACCAGCCCA 540
TGGAGAGGCT CTATGAAGAG CTCGTGGAGC GCATGGAAGC AATGGGGGAG TGGAAACCCCA 600
ATGTCAAGGA GATCAAGGTC CTGCAGAAGA TCGGAAAAGA TACATTCATT ACTCACGAGC 660
TGGCTGCCGA GGCAGCAGGA AACCTGGTGG GGCCCCGTGA CTTTGTGAGC GTGCGCTGTG 720
CCAAGCGCCG AGGCTCCACC TGTGTGCTGG CTGGCATGGC CACAGACTTC GGGAACATGC 780
CTGAGCAGAA GGGTGTCTATC AGGGCGGAGC ACGGTCCCAC TTGCATGGTG CTTACCCCGT 840
TGGCTGGAAG TCCCTCTAAG ACCAAACTTA CGTGGCTACT CAGCATCGAC CTCAAGGGGT 900
GGCTGCCCAA GAGCATCATC AACCAGGTCC TGTCCCAGAC CCAGGTGGAT TTTGCCAACC 960
ACCTGCGCAA GCGCCTGGAG TCCCACCCTG CCTCTGAAGC CAGGTGTTGA agaccagcct 1020
gctgttccca actgtgccca gctgcactgg tacacacgct catcaggaga atccctactg 1080
gaagcctgca agtctaagat ctccatctgg tgacagtggg atgggtgggg ttcgtgttta 1140
gagtatgaca ctaggattca gattggtgaa agtttttagt accaagaaaa cagggatgag 1200
ctcttggatt aaaaggtaac ttcattcact gattagctat gacatgaggg ttcaggcccg 1260
ctaaaaataa ttgtaaaact ttttttctgg gcccttatgt acccacctaa aaccatcttt 1320
aaaatgctag tggctgatat ggggtgtggg gatgctaacc acagggcctg agaagtcttg 1380
ctttatgggc tcaagaatgc catgcgctgg cagtacatgt gcacaaagca gaatctcaga 1440
gggtctctctg cagccctctg ctctctcccg ccgctgcaca gcaacaccac agaacaagca 1500
gcaccccaca gtgggtgcct tccagaaata tagtccaagc tttctctgtg gaaaaagaca 1560
aaactcatta gtagacatgt ttcctattg ctttcatagg caccagtcag aataaagaat 1620
cataattcac acaaaaaaaaa a 1641